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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/495,448A

DATE: 06/05/2003
TIME: 11:15:37

Input Set : A:\50111301_1.TXT
Output Set: N:\CRF4\06052003\I495448A.raw

3 <110> APPLICANT: LAU, Lester F.
5 <120> TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES
7 <130> FILE REFERENCE: 28758/36072
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/495,448A
C--> 10 <141> CURRENT FILING DATE: 2000-01-31
12 <150> PRIOR APPLICATION NUMBER: 09/142,569
13 <151> PRIOR FILING DATE: 1999-04-02
15 <150> PRIOR APPLICATION NUMBER: 60/013,958
16 <151> PRIOR FILING DATE: 1996-03-15
18 <160> NUMBER OF SEQ ID NOS: 34
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1480
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (180)..(1316)
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Mouse cyr61 cDNA coding sequence
34 <400> SEQUENCE: 1
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37 aaggacaccc gcccgcctcg ccctcgccctc accgcactcc gggcgcattt gatcccgctg 120
39 ctcgcggcgt tggcggttct gtgtcgccgc gctcgccccg gttccctctg cgccgcaca 179
41 atg agc tcc agc acc ttc agg acg ctc gct gtc gcc gtc acc ctt ctc 227
42 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
43 1 5 10 15
45 cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gcc tgc cac tgc 275
46 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
47 20 25 30
49 cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cggt gac 323
50 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
51 35 40 45
53 ggc tgc ggc tgc tgt aag gtc tgc gct aaa caa ctc aac gag gac tgc 371
54 Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
55 50 55 60
57 agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc 419
58 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
59 65 70 75 80
61 ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa 467
62 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
63 85 90 95
65 ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc 515

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66	Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser	
67	100				105							110					
69	tcc	cag	ccc	aac	tgt	aaa	cac	cag	tgc	aca	tgt	att	gat	ggc	gcc	gtg	563
70	Phe	Gln	Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val	
71	115				120							125					
73	ggc	tgc	att	cct	ctg	tgt	ccc	caa	gaa	ctg	tct	ctc	ccc	aat	ctg	ggc	611
74	Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly	
75	130				135							140					
77	tgt	ccc	aac	ccc	cg	ctg	gtg	aaa	gtc	agc	ggg	cag	tgc	tgt	gaa	gag	659
78	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Ser	Gly	Gln	Cys	Cys	Glu	Glu	
79	145				150						155			160			
81	tgg	gtt	tgt	gat	gaa	gac	agc	att	aag	gac	tcc	ctg	gac	gac	cag	gat	707
82	Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Ser	Leu	Asp	Asp	Gln	Asp	
83	165				170						175						
85	gac	ctc	ctc	gga	ctc	gat	gcc	tcg	gag	gtg	gag	tta	acg	aga	aac	aat	755
86	Asp	Leu	Leu	Gly	Leu	Asp	Ala	Ser	Glu	Val	Glu	Leu	Thr	Arg	Asn	Asn	
87	180				185						190						
89	gag	tta	atc	gca	att	gga	aaa	ggc	agc	tca	ctg	aag	agg	ctt	cct	gtc	803
90	Glu	Leu	Ile	Ala	Ile	Gly	Lys	Gly	Ser	Ser	Leu	Lys	Arg	Leu	Pro	Val	
91	195				200						205						
93	ttt	ggc	acc	gaa	ccg	cga	gtt	ctt	ttc	aac	cct	ctg	cac	gcc	cat	ggc	851
94	Phe	Gly	Thr	Glu	Pro	Arg	Val	Leu	Phe	Asn	Pro	Leu	His	Ala	His	Gly	
95	210				215						220						
97	cag	aaa	tgc	atc	gtt	cag	acc	acg	tct	tgg	tcc	cag	tgc	tcc	aag	agc	899
98	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Ser	
99	225				230						235			240			
101	tgc	gga	act	ggc	atc	tcc	aca	cga	gtt	acc	aat	gac	aac	cca	gag	tgc	947
102	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Glu	Cys	
103	245				250						255						
105	cgc	ctg	gtg	aaa	gag	acc	cg	atc	tgt	gaa	gtg	cgt	cct	tgt	gga	caa	995
106	Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys	Gly	Gln	
107	260				265						270						
109	cca	gtg	tac	agc	agc	cta	aaa	aag	ggc	aag	aaa	tgc	agc	aag	acc	aag	1043
110	Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	Lys	Thr	Lys	
111	275				280						285						
113	aaa	tcc	cca	gaa	cca	gtc	aga	ttt	act	tat	gca	gga	tgc	tcc	agt	gtc	1091
114	Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Ser	Ser	Val	
115	290				295						300						
117	aag	aaa	tac	cg	ccc	aaa	tac	tgc	ggc	tcc	tgc	gta	gat	ggc	cg	tgc	1139
118	Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	
119	305				310						315			320			
121	tgc	aca	cct	ctg	cag	acc	aga	act	gtg	aag	atg	cg	ttc	cga	tgc	gaa	1187
122	Cys	Thr	Pro	Leu	Gln	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	Arg	Cys	Glu	
123	325				330						335						
125	gat	gga	gag	atg	ttt	tcc	aag	aat	gtc	atg	atg	atc	cag	tcc	tgc	aaa	1235
126	Asp	Gly	Glu	Met	Phe	Ser	Lys	Asn	Val	Met	Met	Ile	Gln	Ser	Cys	Lys	
127	340				345						350						
129	tgt	aac	tac	aac	tgc	ccg	cat	ccc	aac	gag	gca	tcg	ttc	cga	ctg	tac	1283
130	Cys	Asn	Tyr	Asn	Cys	Pro	His	Pro	Asn	Glu	Ala	Ser	Phe	Arg	Leu	Tyr	

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131 355 360 365
133 agc cta ttc aat gac atc cac aag ttc agg gac taagtgcctc cagggttcct 1336
134 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
135 370 375
137 agtgtggct ggacagagga gaagcgcaag catcatggag acgtgggtgg gcggaggatg 1396
139 aatggtgct tgctcattct tgagtagcat tagggtattt caaaactgcc aaggggctga 1456
141 tgtggacgga cagcagcgca gccg 1480
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 379
146 <212> TYPE: PRT
147 <213> ORGANISM: Mus musculus
149 <400> SEQUENCE: 2
150 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
151 1 5 10 15
153 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
154 20 25 30
156 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
157 35 40 45
159 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
160 50 55 60
162 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
163 65 70 75 80
165 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
166 85 90 95
168 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
169 100 105 110
171 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
172 115 120 125
174 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
175 130 135 140
177 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
178 145 150 155 160
180 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
181 165 170 175
183 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
184 180 185 190
186 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
187 195 200 205
189 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
190 210 215 220
192 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
193 225 230 235 240
195 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
196 245 250 255
198 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
199 260 265 270
201 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
202 275 280 285
204 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val

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205 290 295 300
207 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
208 305 310 315 320
210 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
211 325 330 335
213 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
214 340 345 350
216 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
217 355 360 365
219 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
220 370 375
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 1418
225 <212> TYPE: DNA
226 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (124)..(1266)
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Human cyr61 cDNA coding sequence
235 <400> SEQUENCE: 3
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238 tgcacaccag cttgttggcg tcttcgtcgc cgcgcgtgcc ccgggctact cctgcgcgccc 120
240 aca atg agc tcc cgc atc gcc agg gcg ctc gcc tta gtc gtc acc ctt 168
241 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
242 1 5 10 15
244 ctc cac ttg acc agg ctg gcg ctc tcc acc tgc ccc gct gcc tgc cac 216
245 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
246 20 25 30
248 tgc ccc ctg gag gcg ccc aag tgc gcg ccg gga gtc ggg ctg gtc cgg 264
249 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
250 35 40 45
252 gac ggc tgc ggc tgc tgt aag gtc tgc gcc aag cag ctc aac gag gac 312
253 Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
254 50 55 60
256 tgc agc aaa acg cag ccc tgc gac cac acc aag ggg ctg gaa tgc aac 360
257 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
258 65 70 75
260 ttc ggc gcc agc tcc acc gct ctg aag ggg atc tgc aga gct cag tca 408
261 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
262 80 85 90 95
264 gag ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa 456
265 Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
266 100 105 110
268 agt ttc cag ccc aac tgt caa cat cag tgc aca tgt att gat ggc gcc 504
269 Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
270 115 120 125
272 gtg ggc tgc att cct ctg tgt ccc caa gaa cta tct ctc ccc aac ttg 552
273 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu

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274	130	135	140	
276	ggc tgt ccc aac cct cg	gtc aaa gtt acc ggg cag tgc tgc gag		600
277	Gly Cys Pro Asn Pro Arg	Leu Val Lys Val Thr Gly Gln Cys Cys Glu		
278	145	150	155	
280	gag tgg gtc tgt gac gag	gat agt atc aag gac ccc atg gag gac cag		648
281	Glu Trp Val Cys Asp	Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln		
282	160	165	170	175
284	gac ggc ctc ctt ggc aag	gag ctg gga ttc gat gcc tcc gag gtg gag		696
285	Asp Gly Leu Leu Gly	Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu		
286	180	185	190	
288	ttg acg aga aac aat	gaa ttg att gca gtt gga aaa ggc aga tca ctg		744
289	Leu Thr Arg Asn Asn	Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu		
290	195	200	205	
292	aag cgg ctc cct gtt	ttt gga atg gag cct cgc atc cta tac aac cct		792
293	Lys Arg Leu Pro Val	Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro		
294	210	215	220	
296	tta caa ggc cag	aaa tgt att gtt caa aca act tca tgg tcc cag tgc		840
297	Leu Gln Gly Gln	Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys		
298	225	230	235	
300	tca aag acc tgt	gga act ggt atc tcc aca cga gtt acc aat gac aac		888
301	Ser Lys Thr Cys	Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn		
302	240	245	250	255
304	cct gag tgc cgc	ctt gtg aaa gaa acc cgg att tgt gag gtg cgg cct		936
305	Pro Glu Cys Arg	Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro		
306	260	265	270	
308	tgt gga cag cca	gtg tac agc agc ctg aaa aag ggc aag aaa tgc agc		984
309	Cys Gly Gln Pro	Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser		
310	275	280	285	
312	aag acc aag aaa	tcc ccc gaa cca gtc agg ttt act tac gct gga tgt		1032
313	Lys Thr Lys Lys	Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys		
314	290	295	300	
316	ttg agt gtg aag	aaa tac cgg ccc aag tac tgc ggt tcc tgc gtg gac		1080
317	Leu Ser Val Lys	Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp		
318	305	310	315	
320	ggc cga tgc tgc	acg ccc cag ctg acc agg act gtg aag atg cgg ttc		1128
321	Gly Arg Cys Cys	Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe		
322	320	325	330	335
324	cgc tgc gaa gat	ggg gag aca ttt tcc aag aac gtc atg atg atc cag		1176
325	Arg Cys Glu Asp	Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln		
326	340	345	350	
328	tcc tgc aaa tgc	aac tac aac tgc ccg cat gcc aat gaa gca gcg ttt		1224
329	Ser Cys Lys Cys	Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe		
330	355	360	365	
332	ccc ttc tac agg	ctg ttc aat gac att cac aaa ttt agg gac		1266
333	Pro Phe Tyr Arg	Leu Phe Asn Asp Ile His Lys Phe Arg Asp		
334	370	375	380	
336	taaatgtac ctgggttcc	agggcacacc tagacaaaca agggagaaga gtgtcagaat		1326
338	cagaatcatg gagaaaatgg	gcgggggtgg tgtgggtat gggactcatt gtgaaaagga		1386
340	agccttctca ttcttgagga	gcattaaggt at		1418

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date